RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _09/545,998A_

Source: _1Fw16_

Date Processed by STIC: _12/10/04_

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RAW SEQUENCE LISTING   DATE: 12/10/2004
PATENT APPLICATION: US/09/545,998A   TIME: 13:41:47

Input Set : **D:\14094-20005.10 - seq list from client.txt**
Output Set: **N:\CRF4\12102004\I545998A.raw**

SEQUENCE LISTING
```
  4 (1) GENERAL INFORMATION:
  6      (i) APPLICANT: Gorman, Daniel M.
  7                    Randall, Troy D.
  8                    Zlotnik, Albert
 10     (ii) TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
 11                              REAGENTS
 13    (iii) NUMBER OF SEQUENCES: 9
 15     (iv) CORRESPONDENCE ADDRESS:
 16          (A) ADDRESSEE: DNAX Research Institute
 17          (B) STREET: 901 California Avenue
 18          (C) CITY: Palo Alto
 19          (D) STATE: California
 20          (E) COUNTRY: USA
 21          (F) ZIP: 94304-1104
 23      (v) COMPUTER READABLE FORM:
 24          (A) MEDIUM TYPE: Floppy disk
 25          (B) COMPUTER: IBM PC compatible
 26          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 27          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 29     (vi) CURRENT APPLICATION DATA:
```
C--> 30   **(A) APPLICATION NUMBER: US/09/545,998A**
C--> 31   **(B) FILING DATE: 10-Apr-2000**
```
 32          (C) CLASSIFICATION:
 38    (vii) PRIOR APPLICATION DATA:
 35          (A) APPLICATION NUMBER: US 60/023,419
 36          (B) FILING DATE: 16-AUG-1996
 39          (A) APPLICATION NUMBER: US 60/027,901
 40          (B) FILING DATE: 07-OCT-1996
 42   (viii) ATTORNEY/AGENT INFORMATION:
 43          (A) NAME: Ching, Edwin P.
 44          (B) REGISTRATION NUMBER: 34,090
 45          (C) REFERENCE/DOCKET NUMBER: DX0612K
 47     (ix) TELECOMMUNICATION INFORMATION:
 48          (A) TELEPHONE: 650-852-9196
 49          (B) TELEFAX: 650-496-1200
 52 (2) INFORMATION FOR SEQ ID NO: 1:
 54      (i) SEQUENCE CHARACTERISTICS:
 55          (A) LENGTH: 1073 base pairs
 56          (B) TYPE: nucleic acid
 57          (C) STRANDEDNESS: single
 58          (D) TOPOLOGY: linear
 60     (ii) MOLECULE TYPE: cDNA
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63       (ix) FEATURE:
64            (A) NAME/KEY: CDS
65            (B) LOCATION: 68..751
68       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
70  CTCGAGATCC ATTGTGCTGG AAAGGGAACT CCTGAAATCA GCCGACAGAA GACTCAGGAG      60
72  AAGCACT ATG GGG GCA TGG GCC ATG CTG TAT GGA GTC TCG ATG CTC TGT      109
73          Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys
74            1                 5                    10
76  GTG CTG GAC CTA GGT CAG CCG AGT GTA GTT GAG GAG CCT GGC TGT GGC      157
77  Val Leu Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly
78  15                  20                  25                  30
80  CCT GGC AAG GTT CAG AAC GGA AGT GGC AAC AAC ACT CGC TGC TGC AGC      205
81  Pro Gly Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser
82                  35                  40                  45
84  CTG TAT GCT CCA GGC AAG GAG GAC TGT CCA AAA GAA AGG TGC ATA TGT      253
85  Leu Tyr Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys
86              50                  55                  60
88  GTC ACA CCT GAG TAC CAC TGT GGA GAC CCT CAG TGC AAG ATC TGC AAG      301
89  Val Thr Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys
90          65                  70                  75
92  CAC TAC CCC TGC CAA CCA GGC CAG AGG GTG GAG TCT CAA GGG GAT ATT      349
93  His Tyr Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile
94      80                  85                  90
96  GTG TTT GGC TTC CGG TGT GTT GCC TGT GCC ATG GGC ACC TTC TCC GCA      397
97  Val Phe Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala
98  95                  100                 105                 110
100 GGT CGT GAC GGT CAC TGC AGA CTT TGG ACC AAC TGT TCT CAG TTT GGA      445
101 Gly Arg Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly
102                 115                 120                 125
104 TTT CTC ACC ATG TTC CCT GGG AAC AAG ACC CAC AAT GCT GTG TGC ATC      493
105 Phe Leu Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile
106             130                 135                 140
108 CCG GAG CCA CTG CCC ACT GAG CAA TAC GGC CAT TTG ACT GTC ATC TTC      541
109 Pro Glu Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe
110             145                 150                 155
112 CTG GTC ATG GCT GCA TGC ATT TTC TTC CTA ACC ACA GTC CAG CTC GGC      589
113 Leu Val Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly
114     160                 165                 170
116 CTG CAC ATA TGG CAG CTG AGG AGG CAA CAC ATG TGT CCC CGA GAG ACC      637
117 Leu His Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr
118 175                 180                 185                 190
120 CAG CCA TTC GCG GAG GTG CAG TTG TCA GCT GAG GAT GCT TGC AGC TTC      685
121 Gln Pro Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe
122             195                 200                 205
124 CAG TTC CCT GAG GAG GAA CGC GGG GAG CAG ACA GAA GAA AAG TGT CAT      733
125 Gln Phe Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His
126             210                 215                 220
128 CTG GGG GGT CGG TGG CCA TGAGGCCTGG TCTTCCTCTG TGCCCCAAGC           781
129 Leu Gly Gly Arg Trp Pro
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130        225
132 CAGACGCTAC AAGACTTGCC CAGCTATACC CTTGGTGAGA GCAGGGGCCA TGCTCTGCAC      841
134 CCTTCCCTGG GCCTGGCCCT GCTCCCCTCA ACAGTGGCGG AAGTGGGTGT ATGAGAGCGG      901
136 TGAGTTACGA TTGGGCCCTA TGGCTGCCTT TCTCATTTGA CAGCTCTGTT GGAGTAGGGT      961
138 CTTTGGGCCC ACCAAGAGCA CCACGTTTAG CACAAGATCT TGTACAAGAA TAAATACTTG     1021
140 TTTAGTAACC TGAAAAAAAA AAAAAAAAGG GCGGCCGCGG AGGCCGAATT CC             1073
143 (2) INFORMATION FOR SEQ ID NO: 2:
145      (i) SEQUENCE CHARACTERISTICS:
146          (A) LENGTH: 228 amino acids
147          (B) TYPE: amino acid
148          (D) TOPOLOGY: linear
150      (ii) MOLECULE TYPE: protein
152      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
154 Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys Val Leu
155  1               5              10                 15
157 Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly Pro Gly
158          20              25              30
160 Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser Leu Tyr
161          35              40              45
163 Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys Val Thr
164      50              55              60
166 Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys His Tyr
167 65              70                 75                 80
169 Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile Val Phe
170              85              90                 95
172 Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala Gly Arg
173          100             105             110
175 Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly Phe Leu
176          115             120             125
178 Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile Pro Glu
179      130             135             140
181 Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe Leu Val
182 145             150             155             160
184 Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly Leu His
185              165             170             175
187 Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr Gln Pro
188          180             185             190
190 Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe Gln Phe
191          195             200             205
193 Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His Leu Gly
194      210             215             220
196 Gly Arg Trp Pro
197 225
199 (2) INFORMATION FOR SEQ ID NO: 3:
201      (i) SEQUENCE CHARACTERISTICS:
202          (A) LENGTH: 1006 base pairs
203          (B) TYPE: nucleic acid
204          (C) STRANDEDNESS: single
205          (D) TOPOLOGY: linear
```

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207      (ii)  MOLECULE TYPE: cDNA
210      (ix)  FEATURE:
211            (A)  NAME/KEY: CDS
212            (B)  LOCATION: 1..723
215      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 3:
217 ATG GCA CAG CAC GGG GCG ATG GGC GCG TTT CGG GCC CTG TGC GGC CTG        48
218 Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
219  1               5                   10                  15
221 GCG CTG CTG TGC GCG CTC AGC CTG GGT CAG CGC CCC ACC GGG GGT CCC        96
222 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
223             20                  25                  30
225 GGG TGC GGC CCT GGG CGC CTC CTG CTT GGG ACG GGA ACG GAC GCG CGC       144
226 Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
227             35                  40                  45
229 TGC TGC CGG GTT CAC ACG ACG CGC TGC TGC CGC GAT TAC CCG GGC GAG       192
230 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
231         50                  55                  60
233 GAG TGC TGT TCC GAG TGG GAC TGC ATG TGT GTC CAG CCT GAA TTC CAC       240
234 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
235  65                  70                  75                  80
237 TGC GGA GAC CCT TGC TGC ACG ACC TGC CGG CAC CAC CCT TGT CCC CCA       288
238 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
239             85                  90                  95
241 GGC CAG GGG GTA CAG TCC CAG GGG AAA TTC AGT TTT GGC TTC CAG TGT       336
242 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
243             100                 105                 110
245 ATC GAC TGT GCC TCG GGG ACC TTC TCC GGG GGC CAC GAA GGC CAC TGC       384
246 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
247         115                 120                 125
249 AAA CCT TGG ACA GAC TGC ACC CAG TTC GGG TTT CTC ACT GTG TTC CCT       432
250 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
251         130                 135                 140
253 GGG AAC AAG ACC CAC AAC GCT GTG TGC GTC CCA GGG TCC CCG CCG GCA       480
254 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
255 145                 150                 155                 160
257 GAG CCG CTT GGG TGG CTG ACC GTC GTC CTC CTG GCC GTG GCC GCC TGC       528
258 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
259             165                 170                 175
261 GTC CTC CTC CTG ACC TCG GCC CAG CTT GGA CTG CAC ATC TGG CAG CTG       576
262 Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
263             180                 185                 190
265 AGG AGT CAG TGC ATG TGG CCC CGA GAG ACC CAG CTG CTG CTG GAG GTG       624
266 Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val
267             195                 200                 205
269 CCG CCG TCG ACC GAA GAC GCC AGA AGC TGC CAG TTC CCC GAG GAA GAG       672
270 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu
271         210                 215                 220
273 CGG GGC GAG CGA TCG GCA GAG GAG AAG GGG CGG CTG GGA GAC CTG TGG       720
274 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
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275 225                    230              235                240
277 GTG TGAGCCTGGC CGTCCTCCGG GGCCACCGAC CGCAGCCAGC CCCTCCCCAG              773
278 Val
281 GAGCTCCCCA GGCCGCAGGG GCTCTGCGTT CTGCTCTGGG CCGGGCCCTG CTCCCCTGGC       833
283 AGCAGAAGTG GGTGCAGGAA GGTGGCAGTG ACCAGCGCCC TGGACCATGC AGTTCGGCGG       893
285 CCGCTCTAAA GGATCCAAGC TTACGTACGC GTGCATGCGA CGTCATAGCT CTTCTATAGT       953
287 GTCACCTAAA TTCAATTCAC TGGCCGTCGT TTTACAACGT CCTGACTGGG AAA             1006
```

290 (2) INFORMATION FOR SEQ ID NO: 4:
292   (i) SEQUENCE CHARACTERISTICS:
293   (A) LENGTH: 241 amino acids
294   (B) TYPE: amino acid
295   (D) TOPOLOGY: linear
297   (ii) MOLECULE TYPE: protein
299   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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301 Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
302  1               5              10                  15
304 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
305              20              25                  30
307 Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
308          35              40                  45
310 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
311      50                  55                  60
313 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
314  65                  70                  75                  80
316 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
317                  85                  90                  95
319 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
320              100             105                 110
322 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
323          115             120                 125
325 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
326      130                 135                 140
328 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
329 145             150                 155                 160
331 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
332              165                 170                 175
334 Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
335              180                 185                 190
337 Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val
338          195                 200                 205
340 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu
341      210                 215                 220
343 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
344 225             230                 235                 240
346 Val
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349 (2) INFORMATION FOR SEQ ID NO: 5:
351   (i) SEQUENCE CHARACTERISTICS:
352   (A) LENGTH: 723 base pairs
353   (B) TYPE: nucleic acid

VERIFICATION SUMMARY   DATE: 12/10/2004
PATENT APPLICATION: **US/09/545,998A**   TIME: 13:41:48

Input Set : **D:\14094-20005.10 - seq list from client.txt**
Output Set: **N:\CRF4\12102004\I545998A.raw**

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]